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RN [1]
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lersch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and
  2.";
RL J. Biol. Chem. 257:2420-2426(1982).
CC -i- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
CC OF HEAVY-METAL IONS.
CC -i- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR: A03284; SMDZS.
DR HSSP: P55949; IDMF.
DR INTERPRO: IPRO02045; -.
DR INTERPRO: IPRO03019; -.
DR PRAM: PF00131; metalthio: 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28
FT METAL 29 57 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 57 AA; 6109 MW; 8C2B3F6A6BAA3611 CRC64;
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Query Match 88.2%; Score 67; DB 1; Length 57;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CXXCXXCXXCXXCXXCXXCXXCXXCXX 27
DB 30 CEQCSSGCKCANKEDCKRTCSKPCSC 56
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RESULT 5
MTL_HOMAM STANDARD; PRT; 58 AA.
AC P29499;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (CUMT-1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropidae; Nephropidae; Homarus.
RN [1]
RP SEQUENCE.
RX TISSUE=HEPATOPANCREAS;
RX MEDLINE=89215793; PubMed=2709004;
RA Brower M., Winge D.R., Gray W.R.;
RT "Structural and functional diversity of copper-metallothioneins from
  the American lobster Homarus americanus.";
RL J. Inorg. Biochem. 35:289-303(1989).
RN [2]
RP STRUCTURE BY NMR.
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RX MEDLINE=94318629; PubMed=8043573;
RA Zhu Z., Derose E.F., Mullen G.P., Petering D.H., Shaw C.F. III;
RT "Sequential proton resonance assignments and metal cluster topology
  of lobster metallothionein-1.";
RL Biochemistry 33:8858-8865(1994).
CC -i- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF
CC LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.
CC CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION
CC OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN
CC TO BIND CADMIUM.
CC -i- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR: A37039; A37039.
DR HSSP: P55949; IDMF.
DR INTERPRO: IPRO02045; -.
DR INTERPRO: IPRO03019; -.
DR PRAM: PF00131; metalthio: 1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 28
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 5975 MW; 176ABA6F60A32F96 CRC64;
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Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CXXCXXCXXCXXCXXCXXCXXCXXCXX 27
DB 30 CERCTSGCKCPSKDECAKTCSPCSC 56
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RESULT 6
MTL_SCYSE STANDARD; PRT; 58 AA.
AC P02805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (MT-1).
OS Scyllia serrata (Mud Crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunidae; Portunidae; Scylla.
RN [1]
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Lersch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and
  2.";
RL J. Biol. Chem. 257:2420-2426(1982).
CC -i- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
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OF HEAVY-METAL IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR: A03283; SMKDIS.
DR HSSP: P55949; 1DMF.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 6001 MM; CE8A24C590B027B8 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXCXXXXXXCXXXXX 27
DB 30 CEKCSGCKCANKECKSKTCSKACSCC 56

RESULT 7
MT2_CALSI
ID MT2_CALSI STANDARD: PRT: 58 AA.
AC P55950;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunodea; Portunidae; Callinectes.
RN [1]
RP SEQUENCE.
RX MEDLINE-96033062; PubMed-7487904;
RA Browner M., Enghild J., Hoexum-Brouwer T., Thogersen I., Truncali A.;
RT "Primary structure and tissue-specific expression of blue crab
(Callinectes sapidus) metallothionein isoforms.";
Biochem. J. 311:617-622(1995).
CC -1- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP: P55949; 1DMF.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 29 BETA.
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.

FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
SQ SEQUENCE 58 AA; 6287 MM; EF679CB94975C5F0 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXCXXXXXXCXXXXX 27
DB 31 CDKCSSECKCTSKCKSKTCSKPCSCC 57

RESULT 8
MT_ASTFL
ID MT_ASTFL STANDARD: PRT: 58 AA.
AC P55951;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Astacus fluviatilis (Broad-fingered crayfish) (Astacus astacus).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Astacidae; Astacus.
RN [1]
RP SEQUENCE.
RX TISSUE-MIDGUT;
MEDLINE-97079279; PubMed-8921011;
RA Pedersen S.N., Pedersen K.L., Hoelrup P., Depledge M.H., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with
special emphasis on freshwater and semi-terrestrial species.";
Biochem. J. 319:999-1003(1996).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- MASS SPECTROMETRY: MH=5910.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP: P55949; 1DMF.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 BETA.
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.

FT	METAL	31	31	CLUSTER A.
FT	METAL	38	38	CLUSTER A.
FT	METAL	40	40	CLUSTER A.
FT	METAL	46	46	CLUSTER A.
FT	METAL	50	50	CLUSTER A.
FT	METAL	54	54	CLUSTER A.
FT	METAL	56	56	CLUSTER A.
FT	VARIANT	57	57	CLUSTER A.
FT	VARIANT	1	1	MISSING (IN VARIANT ISOLATED IN LOW CADMIUM CONCENTRATION).
SQ	SEQUENCE	58 AA:	5911 MW:	576365B3E5C7122 CRC64;
Query Match				
Best Local Similarity		88.2%;	Score 67;	DB 1; Length 58;
Matches		5; Conservative	18.5%; Pred. No. 23;	22; Mismatches
Oy	1 CXXCXKXXXXXXXKXKXKX 27	:	:	:
Db	31 CDKCTSGCKPSKECAKTCSPCECC 57	:	:	:
RESULT 9				
ID	MT_CARMA	STANDARD:	PRT:	58 AA.
AC	P55948:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	METALLOTHIONEIN (MT).			
OS	Carcinus maenas (Common shore crab) (Green crab).			
OC	Eunaryotia; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eurarchyura; Portunoidea; Portunidae; Carcinus.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=MIDGUT;			
RX	MEDLINE=94153337; PubMed=8110201;			
RA	Pedersen K.L., Pedersen S.N., Hoejrup P., Andersen J.S.,			
RA	Roesporoff P., Knudsen J., Depledge M.H.;			
RT	"Purification and characterization of a cadmium-induced			
RL	bioallothionein from the shore crab Carcinus maenas (L.).";			
Biochem. J.	297:609-614(1994).			
-I-	FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE			
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTs IN MARINE				
CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS				
OF HEAVY-METAL IONS.				
-I-	INDUCTION: BY CADMIUM.			
CC	-I- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.			
DR	HSSP; P55949; 1MD.			
DR	INTERPRO: IPR002045; -			
DR	INTERPRO: IPR003019; -			
PFAM: PF00131;	metalbio; 1.			
DR	PRINTS; PR00858; MTRCRUSTACEAN.			
KW	Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.			
FT	DOMAIN	1	29	BETA.
FT	FT DOMAIN	30	58	ALPHA.
FT	METAL	5	5	CLUSTER B.
FT	METAL	6	6	CLUSTER B.
FT	METAL	10	10	CLUSTER B.
FT	METAL	12	12	CLUSTER B.
FT	METAL	17	17	CLUSTER B.
FT	METAL	21	21	CLUSTER B.
FT	METAL	23	23	CLUSTER B.
FT	METAL	26	26	CLUSTER B.
FT	METAL	28	28	CLUSTER B.
FT	METAL	31	31	CLUSTER A.
FT	METAL	34	34	CLUSTER A.
FT	METAL	38	38	CLUSTER A.
FT	METAL	40	40	CLUSTER A.
FT	METAL	46	46	CLUSTER A.
FT	METAL	50	50	CLUSTER A.

FT	METAL	54	54	CLUSTER A.
FT	METAL	56	56	CLUSTER A.
FT	METAL	57	57	CLUSTER A.
FT	VARIANT	1	1	MISSING (IN VARIANT ISOLATED IN LOW CADMIUM CONCENTRATION).
SQ	SEQUENCE	58 AA;	6133 MW;	0167CDA2B9C9731D CRC64;

Query Match	88.24;	Score 67;	DB 1;	Length 58;
Best Local Similarity	18.5%;	Pred. No. 23;		
Matches	5; Conservative	22; Mismatches	0; Indels	0; Gaps

OY	1	CXXCXXXXXXXXXXXXXCCXXX 27	
Dd	31	CEKSSGCKCTTKEDCCXTKPCSC 57	

RESULT 10				
ID	MT_POTPO	STANDARD;	PRT;	58 AA.
AC	P55952;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	METALLOTHIONEIN (MT).			
OS	Potamon potamios.			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Ploceymata; Brachyura;			
OC	Eubrachyura; Portunoidae; Geonyidae; Potamon.			
RN	[1]			
RP	SEQUENCE.			
RA	TISSUE=MIDGUT;			
RC	MEDLINE=97079279; Pubmed=8921011;			
RA	Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;			
RT	"Primary structures of decapod crustacean metallothioneins with special emphasis on freshwater and semi-terrestrial species."			
RL	Biochem. J. 319:999-1003(1996).			
CC	-1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTIS IN CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS.			
CC	-1- INDUCTION: BY CADMIUM.			
CC	-1- MASS SPECTROMETRY: Mw=6156.8; METHOD=MALDI.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.			
DR	HSSP: P55949; IDMD.			
DR	INTERPRO: IPRO02045; -			
DR	INTERPRO: IPRO03019; -			
PRAM:	PF00131; metalthio; 1.			
DR	PRINTS: PR00858; MTRCRUSTAEAN.			
KW	Metal-binding; Metal-chiolate cluster; Chelation; Cadmium.			
FT	DOMAIN	1	29	BETA.
FT	METAL	30	58	ALPHA.
FT	METAL	4	4	CLUSTER B.
FT	METAL	5	5	CLUSTER B.
FT	METAL	10	10	CLUSTER B.
FT	METAL	12	12	CLUSTER B.
FT	METAL	17	17	CLUSTER B.
FT	METAL	21	21	CLUSTER B.
FT	METAL	23	23	CLUSTER B.
FT	METAL	26	26	CLUSTER B.
FT	METAL	28	28	CLUSTER B.
FT	METAL	31	31	CLUSTER A.
FT	METAL	34	34	CLUSTER A.
FT	METAL	38	38	CLUSTER A.
FT	METAL	40	40	CLUSTER A.
FT	METAL	46	46	CLUSTER A.
FT	METAL	50	50	CLUSTER A.
FT	METAL	54	54	CLUSTER A.
FT	METAL	56	56	CLUSTER A.
FT	METAL	57	57	CLUSTER A.
SQ	SEQUENCE	58 AA;	6157 MW;	DCB719ABAD779C CRC64;

	Query Match	88.2%	Score 67;	DB 1;	Length 58;
	Best Local Similarity	18.5%;	Pred. No. 23;		
Matches	5;	Conservative	22;	Mismatches	0;
				Indels	0;
				Gaps	0;
Oy	1 CXCXXCXXXXXXXXXXXXXCCXX	27			
	:: :: :: :: :: :: :: :: ::				
Dd	31 CEKCTSECKSKRECAKNCTKPCSC	57			

			88.2%	Score	67;	DB	1;	Length	59;
			Best Local Similarity	18.5%;	Pred.	No.	23;		
Matches	5;	Conservative	22;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	CXKCCXXCXXXXXXXXXXXXCXKCCXX	27						
Dz	31	CCCCGGGCGATTCGCCTTCTGTGCCG	57						

	RESULT	11								
ID	MTL_CALSI	STANDARD;	PRT;	59 AA.						
AC	p55949;									
DT	01-NOV-1997 (Rel. 35, Created)									
DT	01-NOV-1997 (Rel. 35, last sequence update)									
DE	METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).									
OS	Callinectes sapidus (Blue crab).									
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;									
OC	Eumalacostrata; Eucarida; Decapoda; Pleocyemata; Brachyura;									
CC	Eubranchiura; Portunoidae; Portunidae; Callinectes.									
RN	[1]									
RP	SEQUENCE.									
RA	BROWDER M., Enghild J., Hoexum-Brouwer T., Thøgersen I., Truncali A.;									
RT	"Primary structure and tissue-specific expression of blue crab									
RL	(<i>Callinectes sapidus</i>) metallothionein isoforms."									
BL	Biochem. J. 311:617-622(1995).									
CC	[2]									
CC	STRUCTURE BY NMR.									
RX	MEDLINE=96033062; PubMed=7487904;									
RA	Nerula S.S., Brouwer M., Hua Y., Armitage L.M.:									
RT	"Three-dimensional solution structure of <i>Callinectes sapidus</i>									
RL	metallothionein-I determined by homonuclear and heteronuclear									
CC	magnetic resonance spectroscopy."									
BL	Biochemistry 34:620-631(1995).									
CC	-I- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND CADMIUM.									
CC	CADMIUM.									
DR	-I- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.									
DR	PDB; IDMC; 07-FEB--95.									
DR	PDB; IDMD; 07-FEB--95.									
DR	PDB; IDME; 07-FEB--95.									
DR	INTERPRO: IPRO02045; -									
DR	INTERPRO: IPR003019; -									
DR	PPAM: PFO0131; metalthio. 1.									
DR	PRINTS; PRO0856; MTCRUSTACEN.									
KW	Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium; 3D-structure.									
KM										
FT	DOMAIN	1	29	BETA.						
FT	METAL	30	59	ALPHA.						
FT	METAL	5	5	CLUSTER B.						
FT	METAL	6	6	CLUSTER B.						
FT	METAL	10	10	CLUSTER B.						
FT	METAL	12	12	CLUSTER B.						
FT	METAL	17	17	CLUSTER B.						
FT	METAL	21	21	CLUSTER B.						
FT	METAL	23	23	CLUSTER B.						
FT	METAL	26	26	CLUSTER B.						
FT	METAL	28	28	CLUSTER B.						
FT	METAL	31	31	CLUSTER A.						
FT	METAL	34	34	CLUSTER A.						
FT	METAL	38	38	CLUSTER A.						
FT	METAL	40	40	CLUSTER A.						
FT	METAL	46	46	CLUSTER A.						
FT	METAL	50	50	CLUSTER A.						
FT	METAL	54	54	CLUSTER A.						
FT	METAL	56	56	CLUSTER A.						
FT	METAL	57	57	CLUSTER A.						
FT	VARIANT	1	1	MISSING (IN MT-IA).						
SQ	SEQUENCE	59 AA;	6141 MM;	4398DA9D1A96D34 CRC64;						

RESULT	12			
ID	MS84A_DROME	STANDARD;	PRT;	63 AA.
AC	001642;	09VIA3;		
DT	01-JUL-1993	(Rel. 26, Created)		
DT	01-JUL-1993	(Rel. 26, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	MALE SPECIFIC SPERM PROTEIN MS84DA.			
GN	MS84DA.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OREGON-R;			
RX	MEDLINE=92102953; PubMed=1664716;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abail J.F., Agapayni A., An H.-J., Andrews-pfannkuch C., Baldwin D.,			
RA	Bailliv R.M., Basu A., Baxendale J., Bayraktiroglou I., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Beckman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davensport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Perriere S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.C., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbagman C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mcherson D.,			
RA	Merklow G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,			
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Part V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Silver E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Sivarska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.,			
RT	"The genome sequence of Drosophila melanogaster."			
UL	Science 287:2185-2195(2000).			

```

CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -----
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC -----
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CC -----
DR EMBL: X67703; CAA47937.1; -.
DR EMBL: AE003672; AA054022.1; -.
DR HSSP: P01180; INPO.
DR FLYBASE: FBgn0004175; Mst84D.
KW Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 63 AA; 5806 MW; BF84CDD74CBCEFD3F CRC64;

Query Match 88.2%; Score 67; DB 1; Length 63;
Best Local Similarity 18.5%; Pred. No. 24;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 2 XXXXXXXXXXCCCCXXXCCXXXCC 28
Db 14 GPCGPGCGGCGPGCGGCGGCGGCC 40

RESULT 13
M84D_PROME STANDARD; PRT; 68 AA.
AC 001645;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN MST84D.
GN MSTR84DD
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RC MEDLINE=92102953; PubMed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RA Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster."
RL Mech. Dev. 35:143-151(1991).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -----
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC -----
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CC -----
DR EMBL: X67703; CAA47940.1; -.
DR HSSP: P01180; INPO.
DR FLYBASE: FBgn0004175; Mst84D.
KW Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 68AA; 6480 MW; ZF2BD26128DE3DEF CRC64;

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Query Match Similarity 88.2%; Score 67; DB 1; Length 68;
Best Local Similarity 18.5%; Ref. No. 26;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

1 CXXCXXXCXKXXXXXXXXXXXXXCCXXCXX 27
1:|||||:|||||:|||||:|||||:|||||:
Db 13 CGPCCGPGCCGPGCCGPGCCGPGCCGPC 39

RESULT 14
A6ZF_DROME STANDARD; PRT; 115 AA.
AC 046202;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ACCESSORY GLAND PROTEIN ACP62F.
GN ACP62F.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Epiphytoidae; Drosophilidae; Drosophila.
LN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S; TISSUE=MALE ACCESSORY GLAND;
RX MEDLINE=98135120; PubMed=9474779;
RA Wolfner M.F., Harada H.A., Bertum M.J., Stelick T.J., Kraus K.W.,
RA Kalb J.M., Lung Y.O., Neudam D.M., Park M., Tram U.;
RT "New genes for male accessory gland proteins in Drosophila
RT melanogaster.";
RL Insect Biochem. Mol. Biol. 27:825-834(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglou I., Beasley E.M.,
RA Beeson K.Y., Berens P.V., Berman B.P., Bhargava P., Bolshakov S.,
RA Bokorova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavalieri S., Dahlke C., Davenport L.B., Davies P.,
RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Ferriz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jaitai M., Kalush E., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laiko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., Meled M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murthy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheefel F., Shen H.,
RA Shue B.C., Sidman-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaydas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";

Search completed: March 1, 2001, 16:26:02
Job time: 399 sec

RL Science 287:2185-2195(2000).
CC -1- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES IN
CC MATED FEMALE FLIES.
CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -----
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CC -----
CC EMBL: U85763; AAB96387.1; -
DR EMBL: AE003475; AAF47683.1; -
DR FLYBASE: FBgn020509; ACP62F.
KM Behavior.
SQ SEQUENCE 115 AA; 12570 MW; 4326AA6FC32291D CRC64;

Query Match 88.2%; Score 67; DB 1; Length 115;
Best Local Similarity 18.5%; Pred. No. 37;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 2 XXXXXXXXXX
DB 41 TECPVACPETCEXGNGPCVKMGAPC 67

RESULT 15
VES_RHPV1 STANDARD; PRT; 157 AA.
AC P24834;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PROBABLE E5 PROTEIN.
GN E5.
OS Rhesus papillomavirus type 1 (Rhpv 1).
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91135018; PubMed-1847267;
RA Ostrow R.S., Labresh K.V., Faras A.J.;
RT "Characterization of the complete Rhpv 1 genomic sequence and an
RT integration locus from a metastatic tumor."
RL Virology 181:424-429(1991).
CC -----
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CC -----
CC EMBL: M60184; AAA79315.1; ALT_SEQ.
DR EMBL: M60184; AAA79316.1; ALT_SEQ.
DR PIR: F38503; W5WLR1.
KM Early protein.
SQ SEQUENCE 157 AA; 17398 MW; AC7AA67158844686 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 157;
Best Local Similarity 18.5%; Pred. No. 46;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 2 XXXXXXXXXX
DB 23 VLCKANCCYACKPPFCFCFWLCFCCC 49